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PHD OPPORTUNITY



Genetics & Diversity
of Ornamental plants

Title: Origin and transmission of the polyploidy in roses: *Rosa gallica*, an historical node

Location: UMR IRHS (INRAE, Institut-Agro, University of Angers), Angers- Pays de la Loire – France

Come and discover the fascinating world of the rose and enjoy an enriching research experience as part of the GDO team (Genetics and Diversity of Ornamentals) at the IRHS in Angers (France). You will contribute to a better understanding of the history of the rose and strengthen the foundations on which today's breeders can rely to create fragrant varieties that are resilient in the face of climatic changes.

Abstract of the PhD project:

The diversity of modern roses, represented by thousands of cultivars, is unique in that it arises from both a complex network of interspecific hybridizations (involving 7 to 8 wild species) and consists of plants with different levels of polyploidy. Among the related wild species, *Rosa gallica*, a European allotetraploid species, has transmitted this polyploidy trait to cultivated roses and has brought important traits such as fragrance and hardiness. The main questions addressed in this thesis concern the origin of *R. gallica* and its contribution to cultivated roses throughout the selection process. Using a genomic approach (sequencing and analysis of various genomes), this thesis aims to trace the transmission of polyploidy and structural genome modification, from wild populations to modern roses (joint transmission or not of chromosome sets, possible translocations). The roses selected for genome analysis will be chosen based on their position in the genealogy of cultivated roses and according to hypotheses previously drawn by the research team.

Keywords: Genomics, phylogenomics, polyploidy.

Type of funding: Doctoral contract, VAAME school competition (<https://ed-vaame.doctorat-paysdelaloire.fr/>).

Candidate requirements:

The candidate should have a good knowledge of genetics (population genetics) and genomics (phylogenomics, pangenomics). Knowledge of botany would be an asset. The project will require extensive genomic analyses (bio-analyses) on large datasets (sequences), requiring coding skills in R and Python, as well as a great of rigor.

Deadline for online applications: May, 16th 2025

The PhD profile is online accessible (<https://amethis.doctorat.org/amethis-client/prd/consulter/offre/1456>) with details to candidate.

For more information, you can contact Fabrice Foucher, PhD director (fabrice.foucher@inrae.fr), Alix Pernet (alix.pernet@inrae.fr) and Jérémy Clotault (jérémy.clotault@univ-angers.fr), thesis supervisors.

Detailed description of the project:

Polyploidization has played a key role in the evolution of plant genomes and is a major driver of diversification. The *Rosa* genus (comprising more than 150 species and thousands of cultivars) has exhibited a strong tendency toward polyploidization, both in wild and cultivated populations. *Rosa gallica*, a European tetraploid species, has been selected and cultivated in Europe since Antiquity. During the 19th century, crosses between this European species and diploid Asian roses produced polyploid (tri- and tetraploid) descendants, which gave rise to the modern cultivated roses we know today. *R. gallica* contributed important traits to modern cultivated roses, such as hardiness and fragrance. Understanding which parental species contributed to the *Rosa gallica* genome and which genomic regions were transmitted—both to closely related species (*R. centifolia*, *R. muscosa*, etc.) and to modern roses—will provide deeper insight into the role of polyploidization mechanisms in the evolution of natural species and human selection processes. To achieve this, we can rely on pedigree knowledge and the conservation of roses through vegetative propagation. During the PhD, the two following questions will be developed:

1. Which wild species are at the origin of *R. gallica*? *R. gallica* is assumed to be an allopolyploid species, and various hypotheses have been drawn concerning its ancestral species. To investigate this, we will rely on existing and upcoming resources produced by the team (such as the *R. gallica* genome sequence and the resequencing of wild species). The objective is to identify the wild parent species of *R. gallica* or the descendants of these species that are still present today.

2. Which tetraploid genome segments of *R. gallica* have been transmitted through the pedigree of cultivated roses, leading to modern roses (late 19th century)? We can draw on pedigree hypotheses using an interdisciplinary approach that combines history and genetics to trace the transmission of *R. gallica*'s tetraploid genome segments within the lineage of cultivated roses, ultimately leading to modern roses.

The PhD research program is organized into two scientific questions:

1. To test hypotheses regarding the origin of *Rosa gallica*, different approaches will be developed (SCOTag analysis, single-copy nuclear sequence by haplome, sequencing of potential parents or their descendants, k-mer analyses, and pangenomic analyses). At the beginning of the PhD, careful consideration will be given to the selection of species to be sequenced, as well as the sequencing methods (short or long reads) and the best approaches to adopt.

2. Regarding the contribution of *Rosa gallica* to cultivated roses, a selection of around ten relevant cultivated roses will be chosen based on their position in pedigrees. The resequencing of these roses will enable the reconstruction of their pseudo-chromosomes, tagged with alleles from contributing species, including *R. gallica*.

At the beginning of the PhD, the doctoral student will participate in the high-quality sequencing (obtaining the four haplomes) of *R. gallica*. His/Her main contribution will focus on the study of conserved gene families, which will be useful for analyses related to the origin and contribution of *R. gallica*.

The main approaches developed during the PhD will involve genomics and pangenomics (using PanTools). From a technical perspective, the work will mainly involve DNA extraction and sequencing (short reads, such as Illumina, or more likely long reads, such as ONT or PacBio), which will be carried out on the INRAE GENOMICS platforms.

The PhD student will be able to take advantage of a large set of sequenced genomes (high quality or resequenced) available in public databases, as well as the sequencing data that he/she will produce (part of which is financed via sequencing at the EPGV). A high-quality sequence of *R. gallica* will be available during the first year of the thesis (funding requested). Data from previous thesis work (SCOTag, Clovis Pawula's thesis) will be available from the start of the thesis to initiate work on the origin of *R. gallica*. For genome assembly, the PhD student will be able to rely on collaboration with the CNRGV in Toulouse and the WUR in Wageningen for pangenomic analyses.